

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/572, 696  
Source: JFWP  
Date Processed by STIC: 03/29/2006

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IFWP

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/10/572,696

**DATE:** 03/29/2006  
**TIME:** 09:47:07

**Input Set :** A:\42-000400us sequence final.ST25.txt  
**Output Set:** N:\CRF4\03292006\J572696.raw

3 <110> APPLICANT: Garvan Institute of Medical Research  
 5 <120> TITLE OF INVENTION: Method of modulating bone growth, remodeling and adiposity  
 7 <130> FILE REFERENCE: 42-000400US  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/572,696  
 C--> 9 <141> CURRENT FILING DATE: 2006-03-20  
 9 <160> NUMBER OF SEQ ID NOS: 20  
 11 <170> SOFTWARE: PatentIn version 3.3  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 1180  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: human neuropeptide Y1 receptor  
 19 <220> FEATURE:  
 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (7)..(1161)  
 23 <400> SEQUENCE: 1  
 24 aagctt atg aat tca aca tta ttt tcc cag gtt gaa aat cat tca gtc 48  
 25 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val  
 26 1 5 10  
 28 cac tct aat ttc tca gag aag aat gcc cag ctt ctg gct ttt gaa aat 96  
 29 His Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Ala Phe Glu Asn  
 30 15 20 25 30  
 32 gat gat tgt cat ctg ccc ttg gcc atg ata ttt acc tta gct ctt gct 144  
 33 Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala  
 34 35 40 45  
 36 tat gga gct gtg atc att ctt ggt gtc tct gga aac ctg gcc ttg atc 192  
 37 Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile  
 38 50 55 60  
 40 ata atc atc ttg aaa caa aag gag atg aga aat gtt acc aac atc ctg 240  
 41 Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu  
 42 65 70 75  
 44 att gtg aac ctt tcc ttc tca gac ttg ctt gtc atc atg tgt ctc 288  
 45 Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu  
 46 80 85 90  
 48 ccc ttt aca ttt gtc tac aca tta atg gac cac tgg gtc ttt ggt gag 336  
 49 Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu  
 50 95 100 105 110  
 52 gcg atg tgt aag ttg aat cct ttt gtg caa tgt gtt tca atc act gtg 384  
 53 Ala Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val  
 54 115 120 125  
 56 tcc att ttc tct ctg gtt ctc att gct gtg gaa cga cat cag ctg ata 432  
 57 Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile  
 58 130 135 140  
 60 atc aac cct cga ggg tgg aga cca aat aat aga cat gct tat gta ggt 480

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61	Ile	Asn	Pro	Arg	Gly	Trp	Arg	Pro	Asn	Asn	Arg	His	Ala	Tyr	Val	Gly	
62		145			150							155					
64	att	gct	gtg	att	tgg	gtc	ctt	gct	gtg	gct	tct	tct	ttg	cct	ttc	ctg	528
65	Ile	Ala	Val	Ile	Trp	Val	Leu	Ala	Val	Ala	Ser	Ser	Leu	Pro	Phe	Leu	
66		160				165						170					
68	atc	tac	caa	gta	atg	act	gat	gag	ccg	ttc	caa	aat	gta	aca	ctt	gat	576
69	Ile	Tyr	Gln	Val	Met	Thr	Asp	Glu	Pro	Phe	Gln	Asn	Val	Thr	Leu	Asp	
70	175		180				185					190					
72	gcg	tac	aaa	gac	aaa	tac	gtg	tgc	ttt	gat	caa	ttt	cca	tcg	gac	tct	624
73	Ala	Tyr	Lys	Asp	Lys	Tyr	Val	Cys	Phe	Asp	Gln	Phe	Pro	Ser	Asp	Ser	
74		195				200						205					
76	cat	agg	ttg	tct	tat	acc	act	ctc	ctc	ttg	gtg	ctg	cag	tat	ttt	ggt	672
77	His	Arg	Leu	Ser	Tyr	Thr	Leu	Leu	Leu	Val	Leu	Gln	Tyr	Phe	Gly		
78		210				215						220					
80	cca	ctt	tgt	ttt	ata	ttt	att	tgc	tac	ttc	aag	ata	tat	ata	cgc	cta	720
81	Pro	Leu	Cys	Phe	Ile	Phe	Ile	Cys	Tyr	Phe	Lys	Ile	Tyr	Ile	Arg	Leu	
82		225				230						235					
84	aaa	agg	aga	aac	aac	atg	atg	gac	aag	atg	aga	gac	aat	aag	tac	agg	768
85	Lys	Arg	Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	
86		240				245						250					
88	tcc	agt	gaa	acc	aaa	aga	atc	aat	atc	atg	ctg	ctc	tcc	att	gtg	gta	816
89	Ser	Ser	Glu	Thr	Lys	Arg	Ile	Asn	Ile	Met	Leu	Leu	Ser	Ile	Val	Val	
90		255				260						265			270		
92	gca	ttt	gca	gtc	tgc	tgg	ctc	cct	ctt	acc	atc	ttt	aac	act	gtg	ttt	864
93	Ala	Phe	Ala	Val	Cys	Trp	Leu	Pro	Leu	Thr	Ile	Phe	Asn	Thr	Val	Phe	
94		275				280						285					
96	gat	tgg	aat	cat	cag	atc	att	gct	acc	tgc	aac	cac	aat	ctg	tta	ttc	912
97	Asp	Trp	Asn	His	Gln	Ile	Ile	Ala	Thr	Cys	Asn	His	Asn	Leu	Leu	Phe	
98		290				295						300					
100	ctg	ctc	tgc	cac	ctc	aca	gca	atg	ata	tcc	act	tgt	gtc	aac	ccc	ata	960
101	Leu	Leu	Cys	His	Leu	Thr	Ala	Met	Ile	Ser	Thr	Cys	Val	Asn	Pro	Ile	
102		305				310						315					
104	ttt	tat	ggg	ttc	ctg	aac	aaa	aac	ttc	cag	aga	gac	ttg	cag	ttc	ttc	1008
105	Phe	Tyr	Gly	Phe	Leu	Asn	Lys	Asn	Phe	Gln	Arg	Asp	Leu	Gln	Phe	Phe	
106		320				325						330					
108	tcc	aac	ttt	tgt	gat	ttc	cg	tct	cg	gat	gat	gat	tat	gaa	aca	ata	1056
109	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	
110		335				340						345			350		
112	gcc	atg	tcc	acg	atg	cac	aca	gat	gtt	tcc	aaa	act	tct	ttg	aag	caa	1104
113	Ala	Met	Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	
114		355				360						365					
116	gca	agc	cca	gtc	gca	ttt	aaa	aaa	atc	aac	aat	gat	aat	gaa			1152
117	Ala	Ser	Pro	Val	Ala	Phe	Lys	Lys	Ile	Asn	Asn	Asn	Asp	Asp	Asn	Glu	
118		370				375						380					
120	aaa	atc	tga	aactacttat	agctctaga											1180	
121	Lys	Ile															
125	<210>	SEQ ID NO:	2														
126	<211>	LENGTH:	384														
127	<212>	TYPE:	PRT														

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128 <213> ORGANISM: human neuropeptide Y1 receptor  
 130 <400> SEQUENCE: 2  
 132 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser  
 133 1 5 10 15  
 136 Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp  
 137 20 25 30  
 140 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly  
 141 35 40 45  
 144 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile  
 145 50 55 60  
 148 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val  
 149 65 70 75 80  
 152 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe  
 153 85 90 95  
 156 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met  
 157 100 105 110  
 160 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile  
 161 115 120 125  
 164 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn  
 165 130 135 140  
 168 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala  
 169 145 150 155 160  
 172 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr  
 173 165 170 175  
 176 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr  
 177 180 185 190  
 180 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg  
 181 195 200 205  
 184 Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu  
 185 210 215 220  
 188 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg  
 189 225 230 235 240  
 192 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
 193 245 250 255  
 196 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe  
 197 260 265 270  
 200 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp  
 201 275 280 285  
 204 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu  
 205 290 295 300  
 208 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr  
 209 305 310 315 320  
 212 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Asn  
 213 325 330 335  
 216 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met  
 217 340 345 350  
 220 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser  
 221 355 360 365  
 224 Pro Val Ala Phe Lys Lys Ile Asn Asn Asp Asp Asn Glu Lys Ile

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225 370 375 380  
 228 <210> SEQ ID NO: 3  
 229 <211> LENGTH: 3747  
 230 <212> TYPE: DNA  
 231 <213> ORGANISM: human neuropeptide Y2 receptor  
 234 <220> FEATURE:  
 235 <221> NAME/KEY: CDS  
 236 <222> LOCATION: (496)..(1638)  
 238 <400> SEQUENCE: 3  
 239 gaattcggcc gctgagagac cctggacact gttcctgctc cctcgccacc aaaacttctc 60  
 241 ctccagtccc ctccccgtca ggaccatcgc ccgcaggcctc tgacacctgtt ttcttggttt 120  
 243 taagggtggg gtttgcggcc ctcccccacgc tcccatctct gatcctccca ccttcacccg 180  
 245 cccaccccgcc gagttagtgc ggtgcccagg cgccgttggc ctgagaggtc ggcagcagac 240  
 247 cccgcagcgc caaccggcca gccgctctga ctgctccggc tgccggcccg cgccggcgg 300  
 249 gctgtcctgg acccttaggag gggacggaaac cggacttgcc tttgggcacc ttccaggggcc 360  
 251 ctctccaggt cggctggcta atcatcgac agacggactg cacacatctt gttccgcgt 420  
 253 ctccgcaaaa acgcgagggtc caggtcagtt gtagactctt gtgctgggtt caggccaaagt 480  
 255 ggacctgtac tgaaa atg ggt cca ata ggt gca gag gct gat gag aac cag 531  
 256 Met Gly Pro Ile Gly Ala Glu Ala Asp Glu Asn Gln  
 257 . 1 5 10  
 259 aca gtg gaa gaa atg aag gtg gaa caa tac ggg cca caa aca act cct 579  
 260 Thr Val Glu Glu Met Lys Val Glu Gln Tyr Gly Pro Gln Thr Thr Pro  
 261 15 20 25  
 263 aga ggt gaa ctg gtc cct gac cct gag cca gag ctt ata gat agt acc 627  
 264 Arg Gly Glu Leu Val Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr  
 265 30 35 40  
 267 aag ctg att gag gta caa gtt gtt ctc ata ttg gcc tac tgc tcc atc 675  
 268 Lys Leu Ile Glu Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile  
 269 45 50 55 60  
 271 atc ttg ctt ggg gta att ggc aac tcc ttg gtg atc cat gtg gtg atc 723  
 272 Ile Leu Leu Gly Val Ile Gly Asn Ser Leu Val Ile His Val Val Ile  
 273 65 70 75  
 275 aaa ttc aag agc atg cgc aca gta acc aac ttt ttc att gcc aat ctg 771  
 276 Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu  
 277 80 85 90  
 279 gct gtg gca gat ctt ttg gtg aac act ctg tgt cta ccg ttc act ctt 819  
 280 Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu  
 281 95 100 105  
 283 acc tat acc tta atg ggg gag tgg aaa atg ggt cct gtc ctg tgc cac 867  
 284 Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His  
 285 110 115 120  
 287 ctg gtg ccc tat gcc cag ggc ctg gca gta caa gta tcc aca atc acc 915  
 288 Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr  
 289 125 130 135 140  
 291 ttg aca gta att gcc ctg gac cgg cac agg tgc atc gtc tac cac cta 963  
 292 Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu  
 293 145 150 155  
 295 gag agc aag atc tcc aag cga atc agc ttc ctg att att ggc ttg gcc 1011  
 296 Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala

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297	160	165	170	
299	tgg ggc atc agt gcc ctg ctg gca agt ccc ctg gcc atc ttc cg	gg	1059	
300	Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu			
301	175	180	185	
303	tat tcg ctg att gag atc att ccg gac ttt gag att gtg gcc tgt act		1107	
304	Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr			
305	190	195	200	
307	gaa aag tgg cct ggc gag gag aag agc atc tat ggc act gtc tat agt		1155	
308	Glu Lys Trp Pro Gly Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser			
309	205	210	215	220
311	ctt tct tcc ttg atc ttg tat gtt ttg cct ctg ggc att ata tca		1203	
312	Leu Ser Ser Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser			
313	225	230	235	
315	ttt tcc tac act cgc att tgg agt aaa ttg aag aac cat gtc agt cct		1251	
316	Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro			
317	240	245	250	
319	gga gct gca aat gac cac tac cat cag cga agg caa aaa acc acc aaa		1299	
320	Gly Ala Ala Asn Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys			
321	255	260	265	
323	atg ctg gtg tgt gtg gtg gtg ttt gcg gtc agc tgg ctg cct ctc		1347	
324	Met Leu Val Cys Val Val Val Phe Ala Val Ser Trp Leu Pro Leu			
325	270	275	280	
327	cat gcc ttc cag ctt gcc gtt gac att gac agc cag gtc ctg gac ctg		1395	
328	His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu			
329	285	290	295	300
331	aag gag tac aaa ctc atc ttc aca gtg ttc cac att atc gcc atg tgc		1443	
332	Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys			
333	305	310	315	
335	tcc act ttt gcc aat ccc ctt ctc tat ggc tgg atg aac agc aac tac		1491	
336	Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr			
337	320	325	330	
339	aga aag gct ttc ctc tcg gcc ttc cgc tgt gag cag cgg ttg gat gcc		1539	
340	Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala			
341	335	340	345	
343	att cac tct gag gtg tcc gtg aca ttc aag gct aaa aag aac ctg gag		1587	
344	Ile His Ser Glu Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu			
345	350	355	360	
347	gtc aga aag aac agt ggc ccc aat gac tct ttc aca gag gct acc aat		1635	
348	Val Arg Lys Asn Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn			
349	365	370	375	380
351	gtc taaggaagct gtgggtgtgaa aatgttatgga tgaattctga ccagagctat		1688	
352	Val			
355	aatctgggtt gatggcggtt cacaagtgaa aactgatttc ccattttaaa gaagaagtgg		1748	
357	atctaaatgg aagcatctgc tggttaattc ctggaaaact ggctggcag agcctgtgt		1808	
359	aaaatactgg aattcaaaga taaggcaaca aaatggttt cttAACAGTT ggTTGGGTAG		1868	
361	taggttgcat tatgagtaaa agcagagaga agtactttt attatttcc tggagtgaag		1928	
363	aaaacttgaa caagaaattt gtattatcaa agcattgtcg agagacggtg ggaaaataag		1988	
365	ttgactttca aatcacgtt ggacctggat tgaggaggtg tgcaGTTCGC tgctccctgc		2048	
367	ttggctttagt aaaacaccac tgaacagaaa tttctccagg gagccacagg ctctccctca		2108	

**VERIFICATION SUMMARY**

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Input Set : A:\42-000400us sequence final.ST25.txt  
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date